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The Effect of Shape and Concentration on Translational Diffusion of Proteins Measured by PFG NMR

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Abstract The concentration dependences of self-diffusion coefficient for irregular-shaped fibrinogen, for globular, spheroidal trypsin and α-chymotrypsin were studied by pulsed field gradient nuclear magnetic resonance. The experimental data were analyzed in a view of two known theoretical approaches—the hydrodynamic model of rigid spheres by Tokuyama and Oppenheim and the phenomenological approach based on the frictional formalism of non-equilibrium thermodynamics by Vink. The detailed discussion of their merits and drawbacks is presented. Our results testify that the Vink's approach is quite universal, providing a satisfactory description of experimental data for proteins of complicated structure and different shape while the model of Tokuyama and Oppenheim is applicable only to proteins of more regular shape.

1 Introduction

The diffusion of proteins is of great importance for biological systems. Transport, thermodynamic and functional properties of proteins are bound with their molecular motion. The diffusion coefficient is one of the most important physicochemical characteristics of protein molecule, which provides not only the size and shape data but also information about protein interactions [1–5]. Translational diffusion is a random thermal motion of molecules being the most fundamental form of transport.

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